Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/14 22:58:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153321.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1153321 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153321.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Dec 14 22:58:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153321.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	59,968,462
Mapped reads	59,484,837 / 99.19%
Unmapped reads	483,625 / 0.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	479,210 / 0.8%
Read min/max/mean length	30 / 100 / 100.33
Duplicated reads (estimated)	32,743,398 / 54.6%
Duplication rate	36.03%
Clipped reads	8,470,396 / 14.12%

2.2. ACGT Content

Number/percentage of A's	1,548,230,208 / 26.87%
Number/percentage of C's	1,325,214,278 / 23%
Number/percentage of T's	1,581,106,919 / 27.44%
Number/percentage of G's	1,305,142,112 / 22.65%
Number/percentage of N's	1,587,184 / 0.03%
GC Percentage	45.66%

2.3. Coverage

Mean	1.8614

Standard Deviation	19.1671

2.4. Mapping Quality

Mean Mapping Quality	50.18

2.5. Mismatches and indels

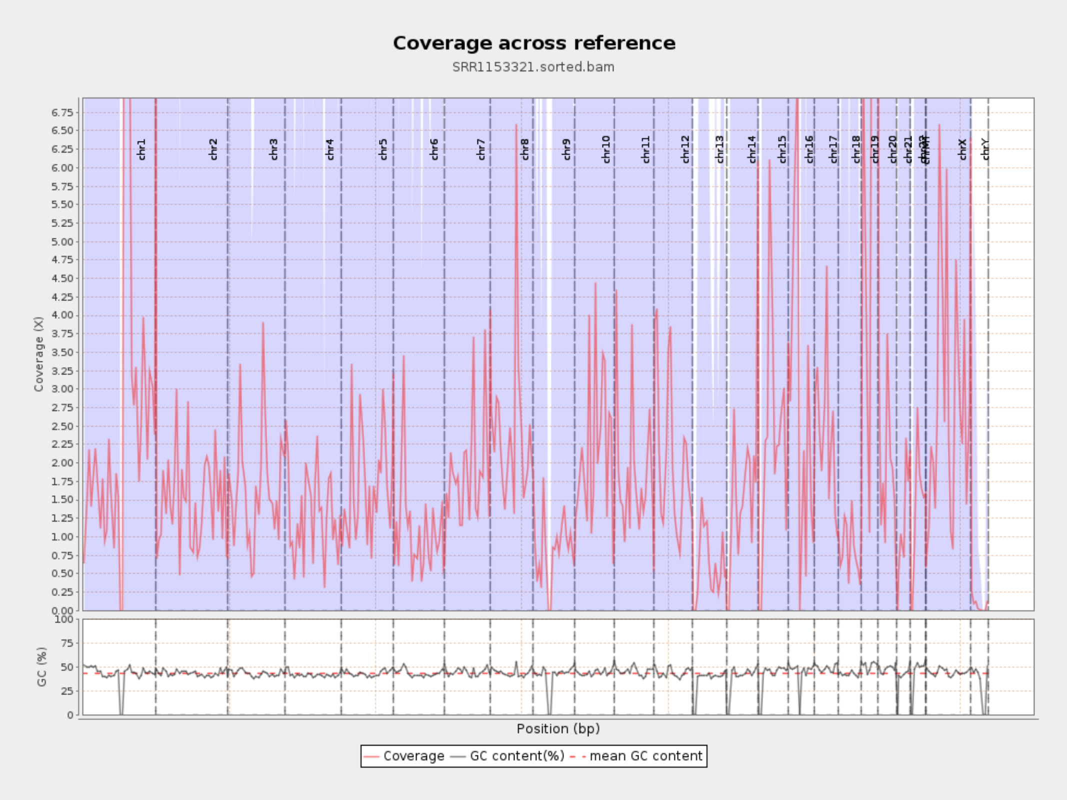
General error rate	0.3%
Mismatches	16,442,854
Insertions	601,646
Mapped reads with at least one insertion	1%
Deletions	469,322
Mapped reads with at least one deletion	0.78%
Homopolymer indels	49.49%

2.6. Chromosome stats

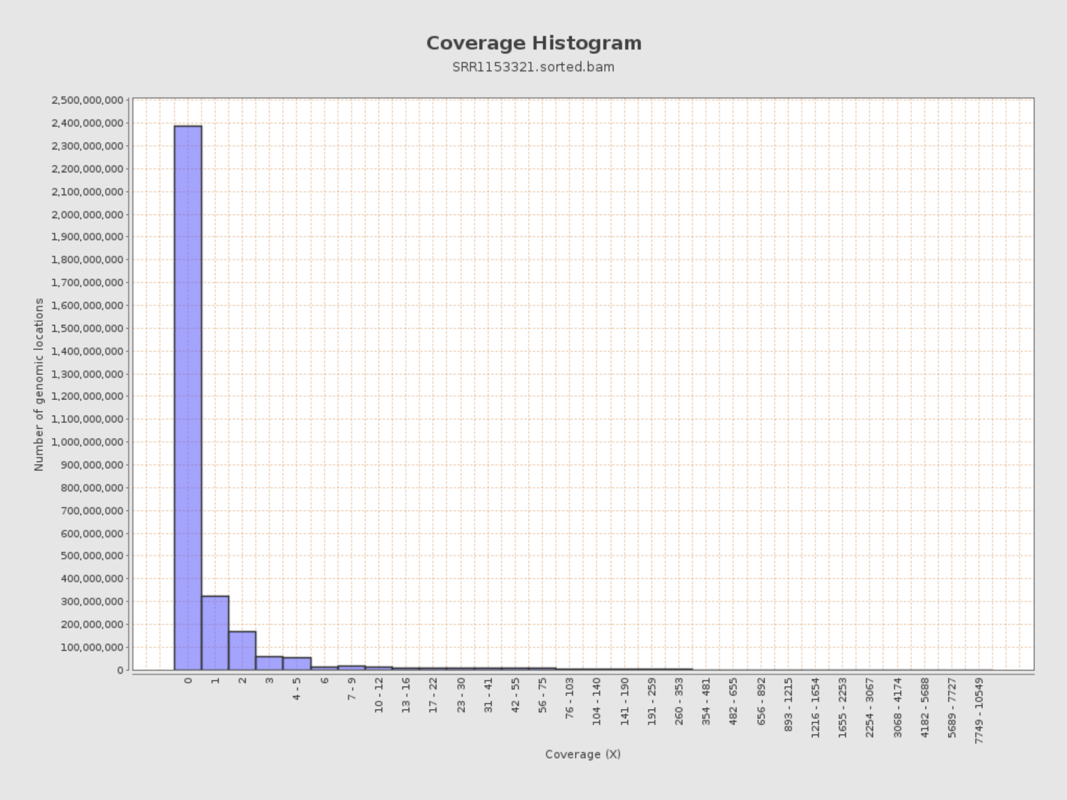
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	691213727	2.7732	28.8717
chr2	243199373	364284549	1.4979	13.2365
chr3	198022430	328452393	1.6587	14.9202
chr4	191154276	252001669	1.3183	13.3383
chr5	180915260	308723843	1.7065	16.0626
chr6	171115067	184095419	1.0759	11.9592
chr7	159138663	295662313	1.8579	18.0387

chr8	146364022	352535573	2.4086	26.1565
chr9	141213431	114742928	0.8125	8.9791
chr10	135534747	302380544	2.231	18.5509
chr11	135006516	255034210	1.8891	16.4472
chr12	133851895	283843553	2.1206	18.0808
chr13	115169878	70654753	0.6135	7.2202
chr14	107349540	161369565	1.5032	14.184
chr15	102531392	229793140	2.2412	20.2775
chr16	90354753	249722776	2.7638	23.7647
chr17	81195210	203004926	2.5002	17.9652
chr18	78077248	65264040	0.8359	10.6022
chr19	59128983	350612237	5.9296	48.3416
chr20	63025520	121411935	1.9264	16.6332
chr21	48129895	60243044	1.2517	12.313
chr22	51304566	69754360	1.3596	13.5547
chrMT	16571	9456	0.5706	1.8645
chrX	155270560	443170995	2.8542	27.3847
chrY	59373566	4273752	0.072	2.9146

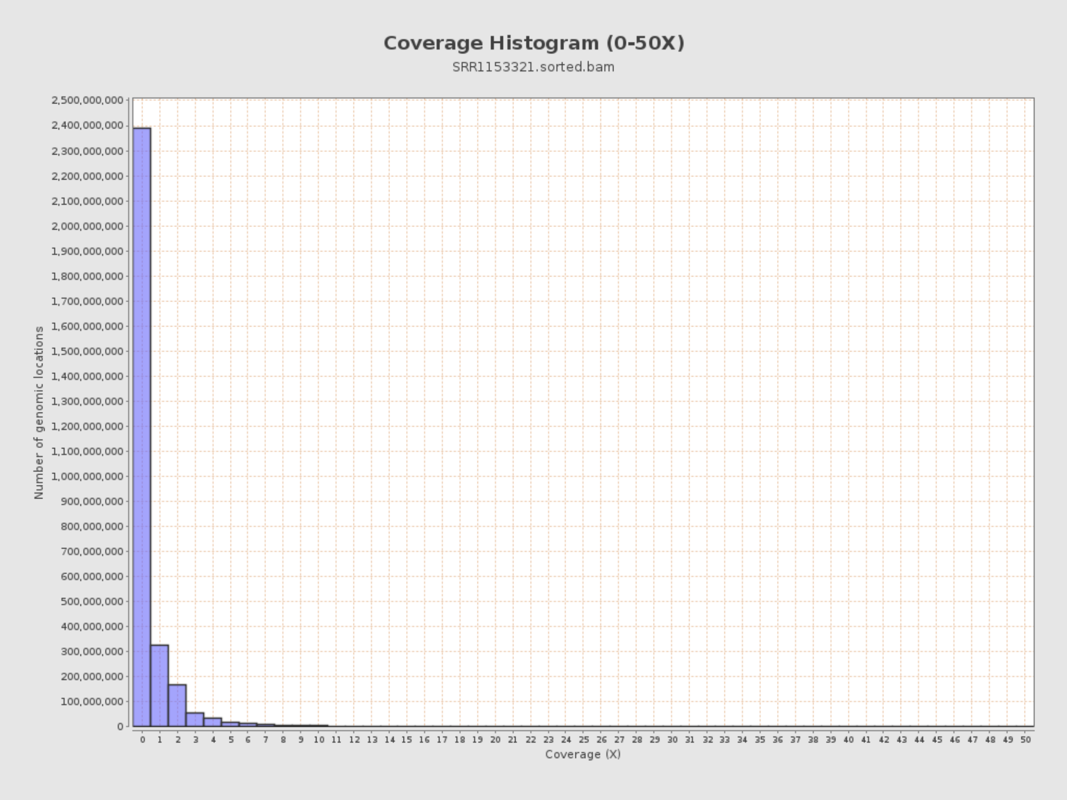
3. Results : Coverage across reference



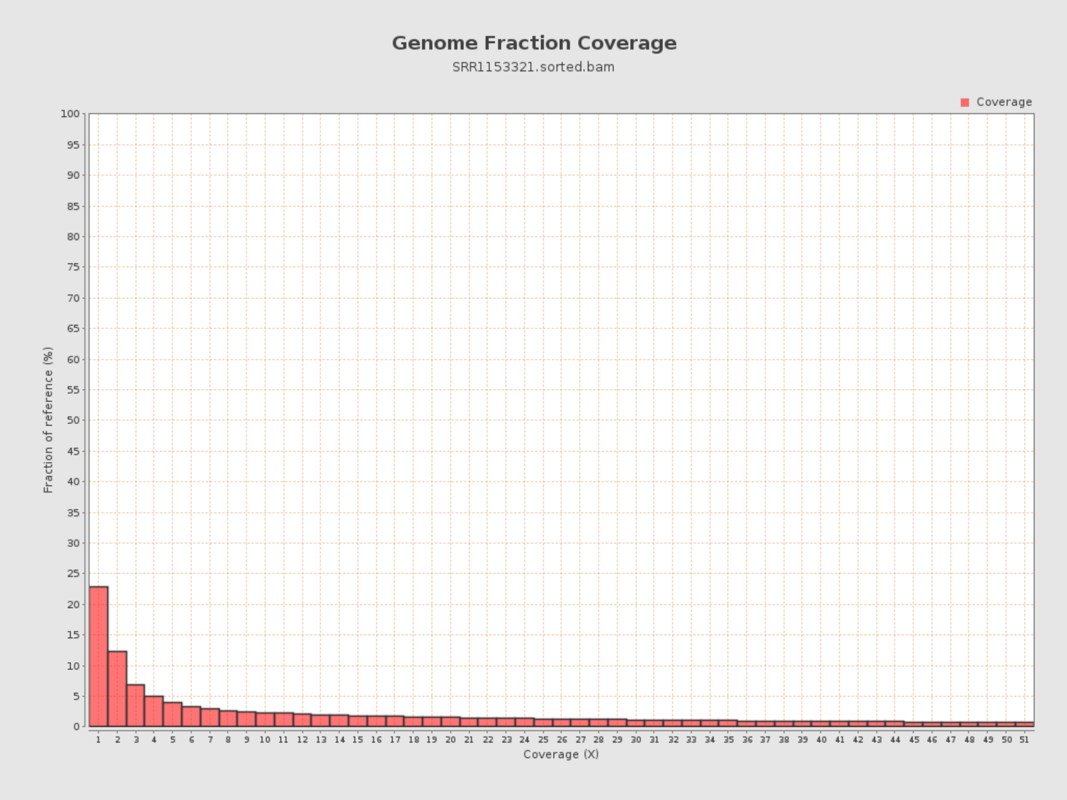
4. Results : Coverage Histogram



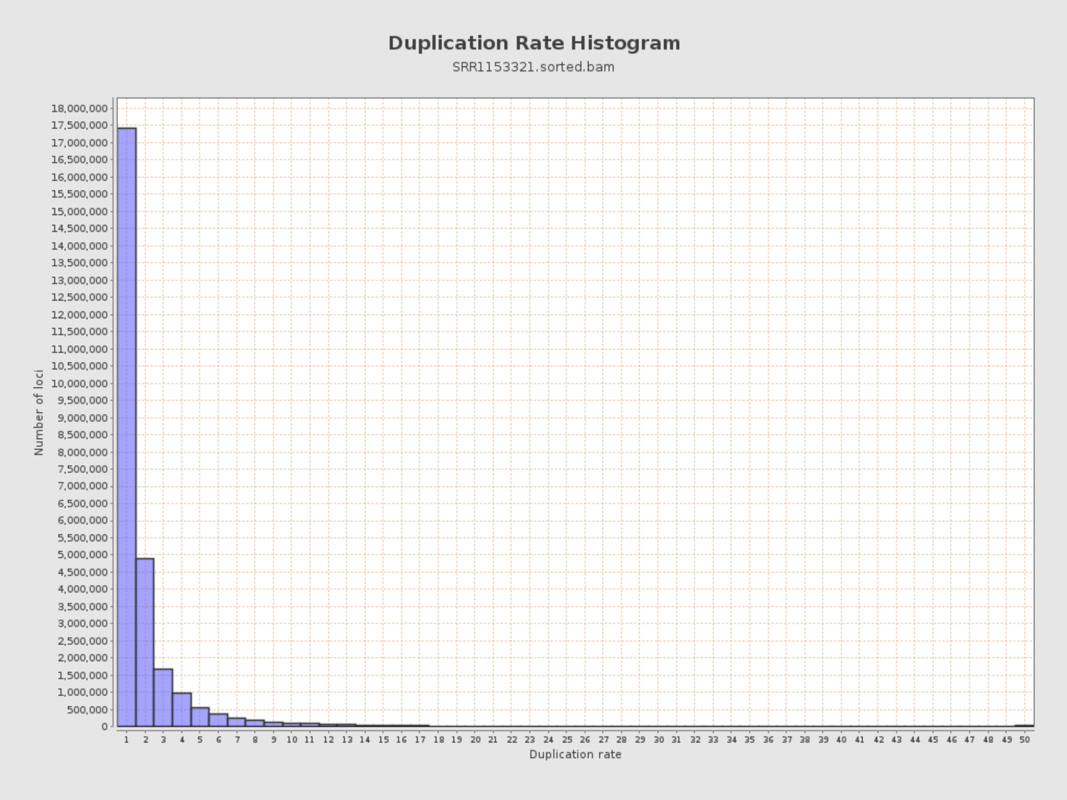
5. Results : Coverage Histogram (0-50X)



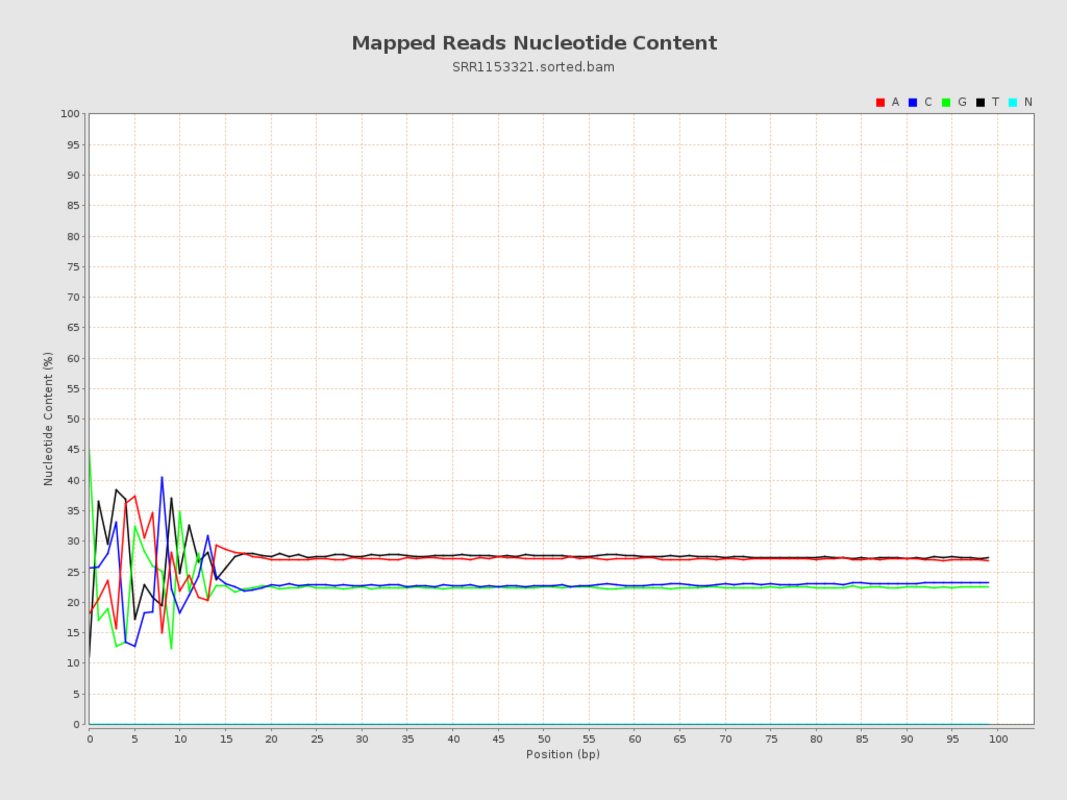
6. Results : Genome Fraction Coverage



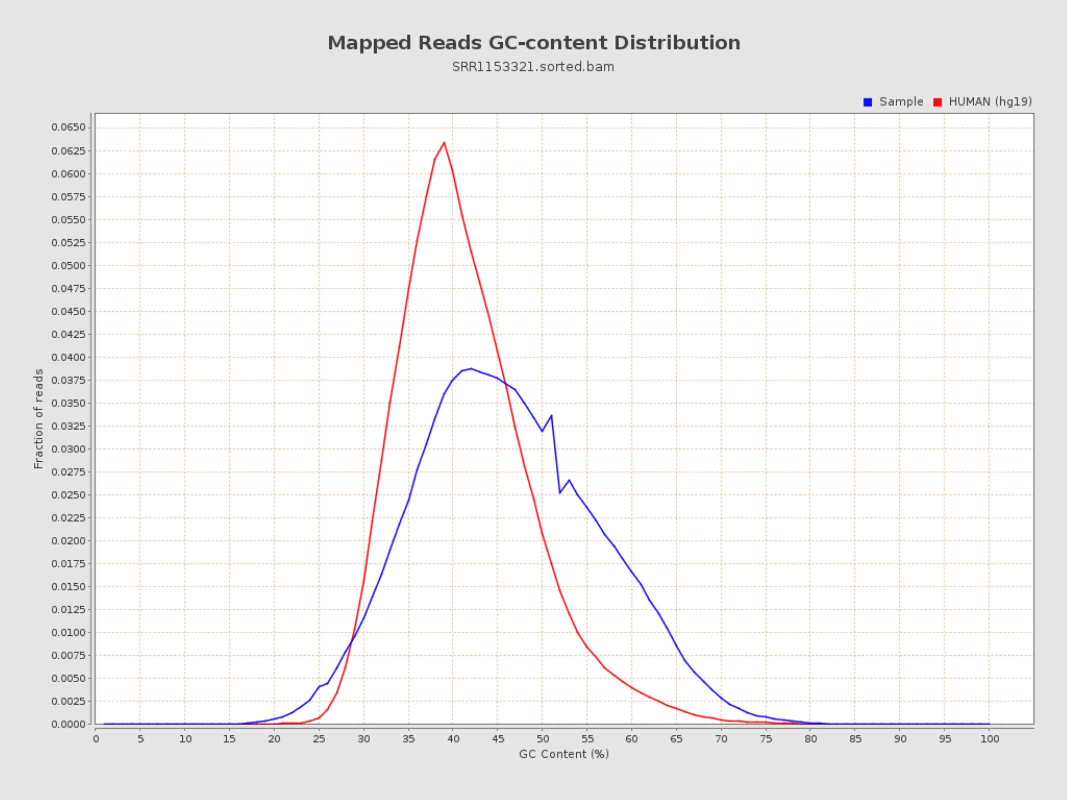
7. Results : Duplication Rate Histogram



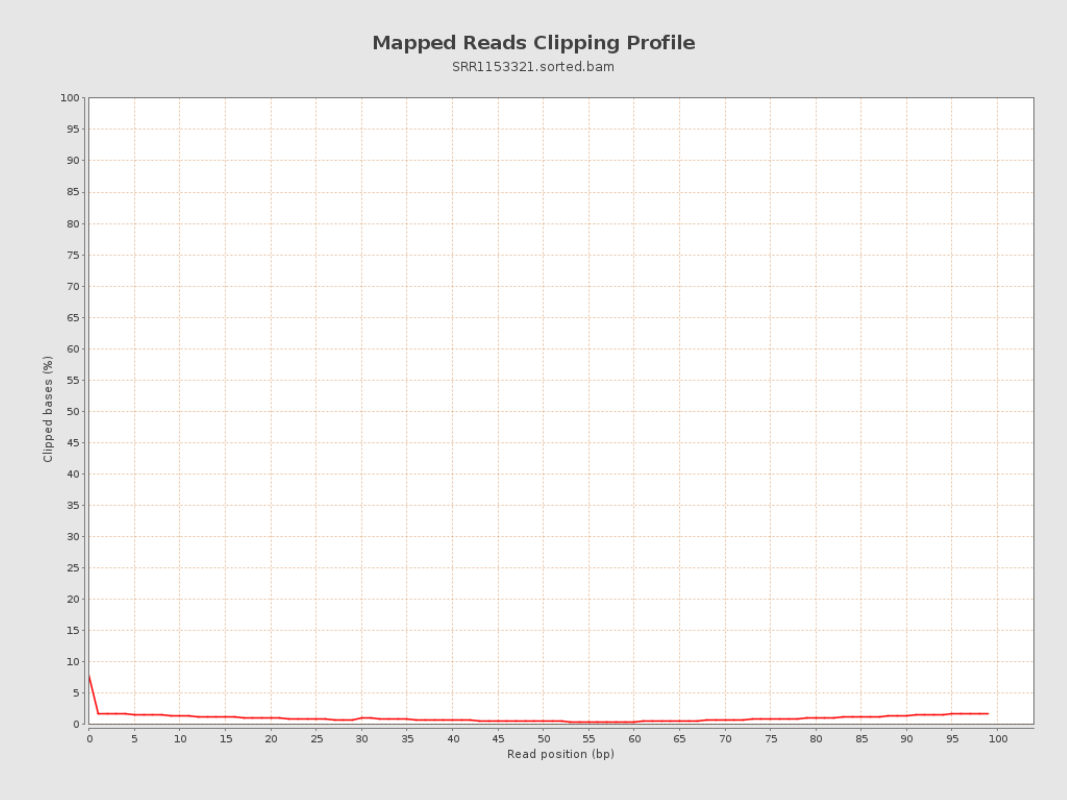
8. Results : Mapped Reads Nucleotide Content



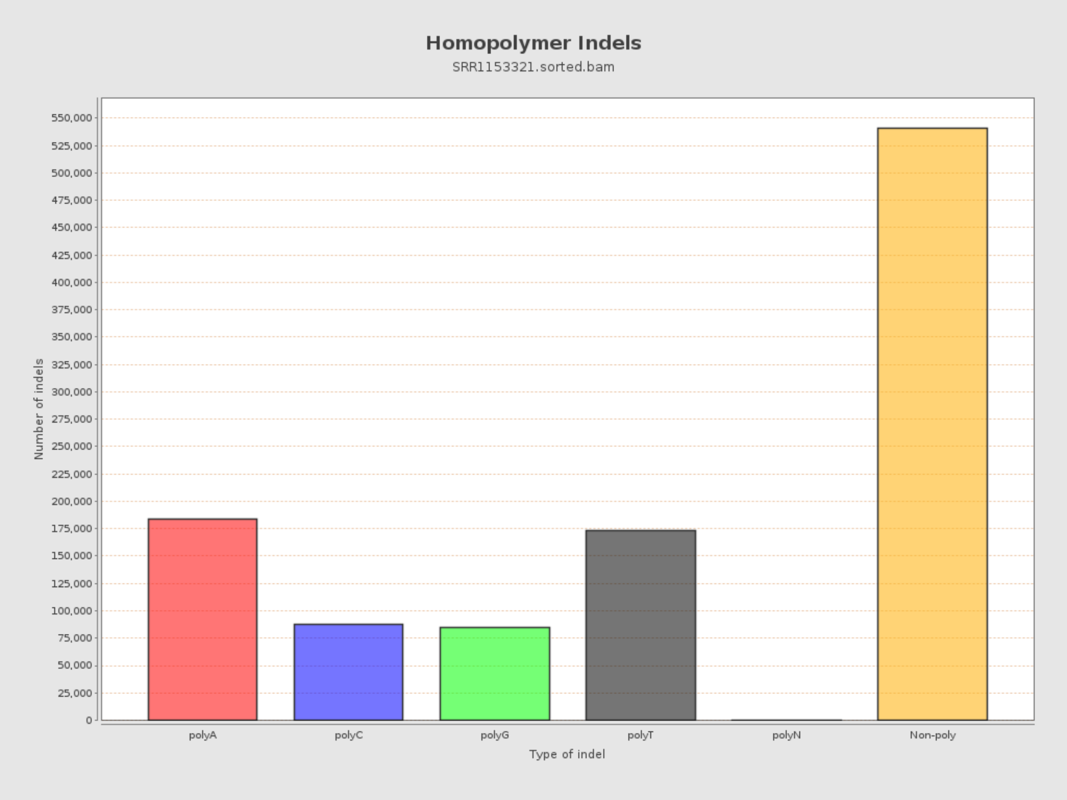
9. Results : Mapped Reads GC-content Distribution



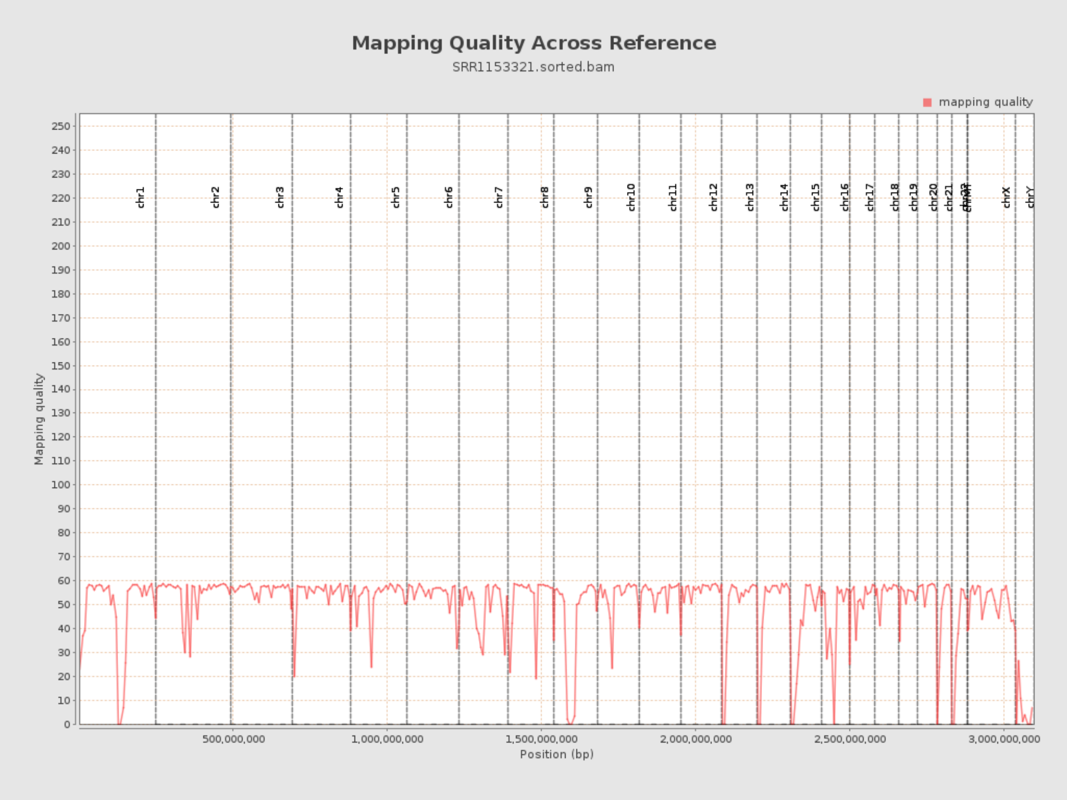
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram